

Exhibit A align10_1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 15:37:11 ; Search time 0.001 Seconds
(without alignments)
679.944 Million cell updates/sec

Title: us-09-674-593-10

Perfect score: 246
Sequence: 1 gtcattaaccttgcgaagga.....ttcatatcaaccacacta 246

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 segs, 1382 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-674-593-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	244.4	99.3	1382	1	us-09-674-593-1

ALIGNMENTS

RESULT 1
us-09-674-593-1

Query Match 99.3%; Score 244.4; DB 1; Length 1382;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	GTGATTAACTTGGCAAGATACCTTTTATTTCTTTAAGATTCCTGTTGTTATACAC	60
DB	268	GTGACTAACCTTGGCAAGATACCTTTTATTTCTTTAAGATTCCTGTTGTTATACAC	327
QY	61	AGATTTTAAGTTACTCTACTACTGACCAAGTAATTCCTTCACGTACAGTGTG	120
DB	328	AGATTTTAAGTTACTCTACTACTGACCAAGTAATTCCTTCACGTACAGTGTG	387
QY	121	AACTCTACCCCGCAAGTGAAGAGATTTTGGAGGAGATCAATGACACCGAAGTCA	180
DB	388	AACTCTACCCCGCAAGTGAAGAGATTTTGGAGGAGATCAATGACACCGAAGTCA	447
QY	181	CAGCCCGTCAACACAGAGAGTGGGGGATGAGATTCGATTTCTCATATCAACCCC	240
DB	448	CAGCCCGTCAACACAGAGTGGGGGATGAGATTCGATTTCTCATATCAACCCC	507
QY	241	ACACTA 246	
DB	508	ACACTA 513	

Search completed: June 4, 2004, 15:37:11
UOD time : 0.001 secs